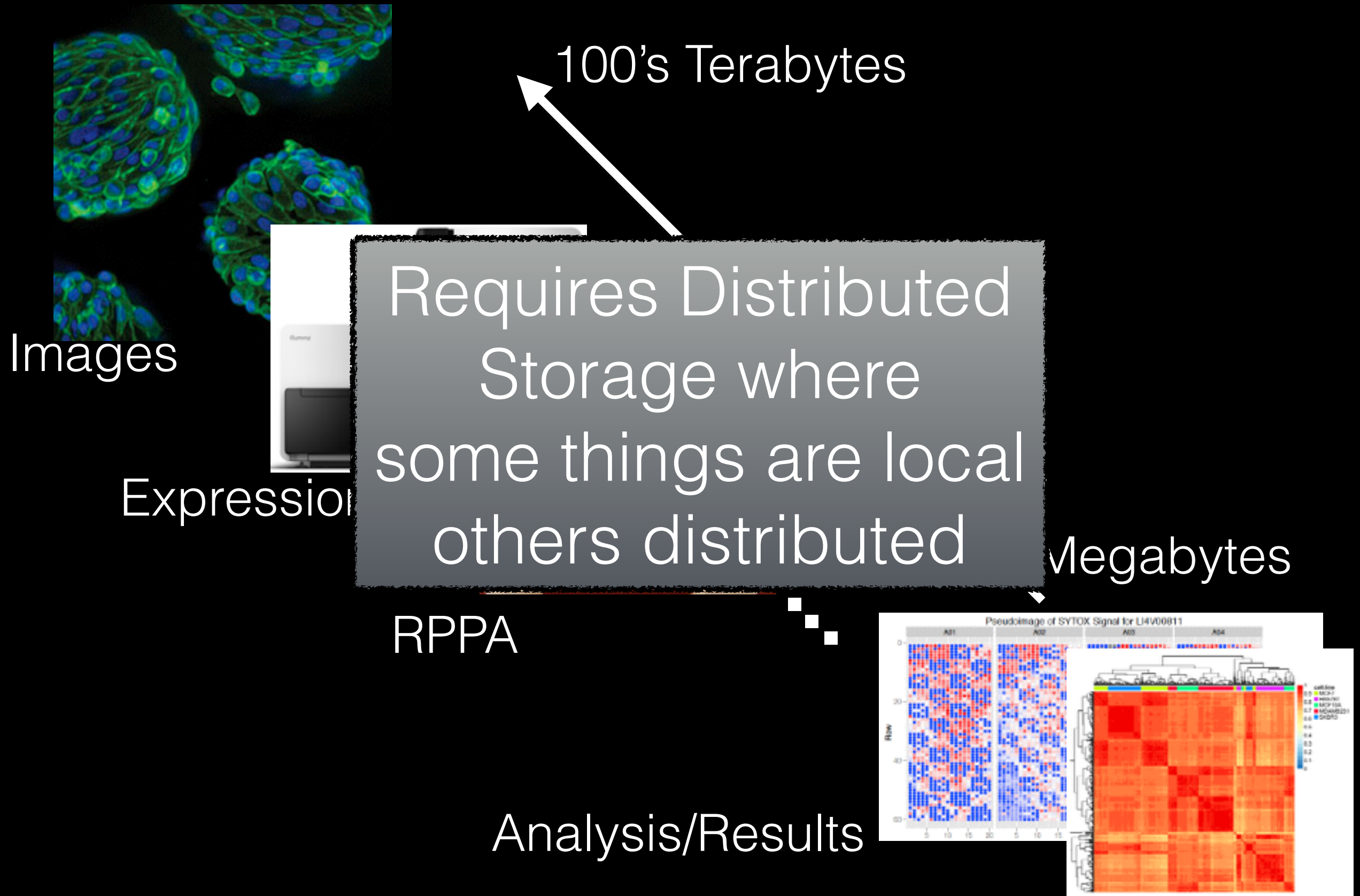


MEP LINCS Knowledge portal: Synapse a brief introduction

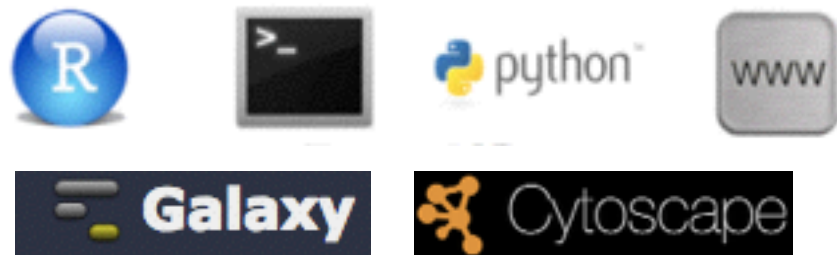
Larsson Omberg
Sage Bionetworks, OHSU LINCS center

Multiple levels of data



Synapse

enabling large-scale collaborative science



Run any tool



On any platform



 Synapse

Record and Share in Synapse

Synapse

enabling large-scale collaborative science

distributed & versioned file system
rich annotations (metadata)
agnostic to storage solution (cloud, local server, etc.)

Strongly typed customizable schemas for structured data

data accessed via any number of 'clients'

www.synapse.org


programmatic clients (R, python, command line)


wiki authoring


access controls (share whatever with whomever)

Synapse


enabling large-scale collaborative science




 **Synapse** CONTRIBUTE to the CURE

Alpha features on [off](#) [Help](#)  Larsson Omberg (larsson0)

 JWGray Breast Cancer Cell Line Panel

[Wiki](#) **[Files](#)** [Tables](#) beta

 [Files](#) » [Baseline_Profiling](#) » [JWGray_BCCL_SNP6](#) » [JWGray_BCCL_SNP6_segment...](#)

 **[JWGray BCCL SNP6 segmented v2 gene level.txt.zip](#)**  

File: JWGray_BCCL_SNP6_segmented_v2_gene_level.txt.zip (733.775 KB - Synapse Storage) [md5](#)

Synapse ID: syn2347007







Conditions for use: None ([change](#)) [report issue](#)


DOI: ([create DOI](#))

Annotations ([show](#))

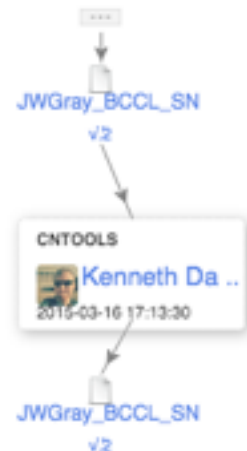
File History ([show](#))

Annotations

dataSubType	cna	
platform	Genome_Wide_SNP_6	
project	JWGray Breast Cancer Cell Line Panel	
dataType	DNA	
species	Homo sapiens	
disease	cancer	

 Add Annotation

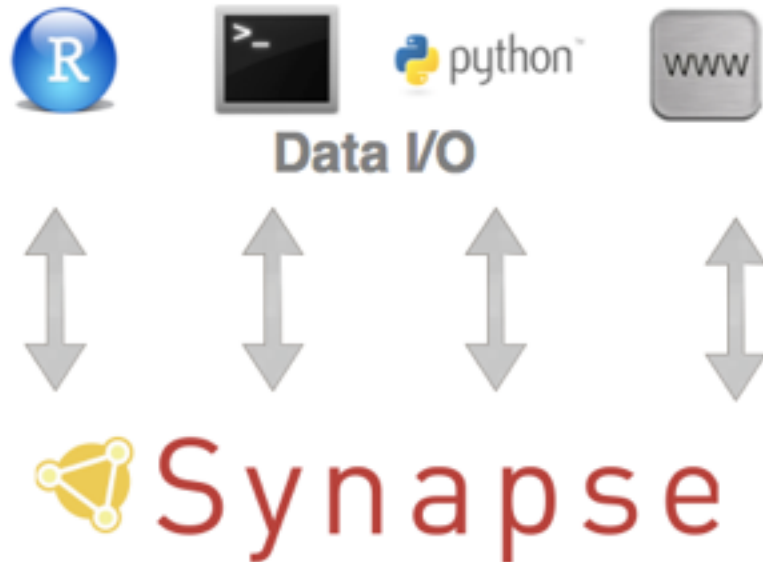
Provenance



```
graph TD; A[JWGray_BCCL_SNP6 v2] --> B[CNTOOLS Kenneth Da .. 2015-03-16 17:13:30]; B --> C[JWGray_BCCL_SNP6 v2];
```

Synapse


enabling large-scale collaborative science




`synapse query select name from file where platform=='Genome_Wide_SNP_6'`





Name	id
broad.mit.edu_COAD_Genome_Wide_SNP_6.hg19.cna_probecount.b	syn2320158
broad.mit.edu_COAD_Genome_Wide_SNP_6.hg19.cna_nocnv_probe	syn2320159
broad.mit.edu_COAD_Genome_Wide_SNP_6.hg19.cna.bed	syn2320161
broad.mit.edu_DLBC_Genome_Wide_SNP_6.hg19.cna_nocnv.bed	syn2320174
broad.mit.edu_LUSC_Genome_Wide_SNP_6.hg19.cna_probecount.b	syn2320177
broad.mit.edu_LUSC_Genome_Wide_SNP_6.hg19.cna_nocnv_prober	syn2320178
JWGray_BCCL_SNP6_segmented_pnas.cbs.txt	syn2346649
JWGray_BCCL_SNP6_segmented_v2.cbs	syn2347005
JWGray_BCCL_SNP6_segmented_v2_gene_level.txt.zip	syn2347007
JWGray_BCCL_SNP6_segmented_v2_table.txt.zip	syn2347009
JWGray_BCCL_SNP6_segmented_v2_table_imputed.txt.zip	syn2347008

Where does a file come from


 **Synapse** CONTRIBUTE to the CURE

[Forum](#)





 **Larsson Omberg (larssono)**




   

Alpha features on [off](#)

 [Progenitor Cell Biology Consortium \(PCBC\)](#)

[Wiki](#) **[Files](#)** [Tables](#)

 [Files](#) »  [C4 Raw Data](#) »  [mRNA](#) »  [bam Files](#) »  [H9.102.2.5.bam](#)

 **[H9.102.2.5.bam](#)**  

File: H9.102.2.5.bam (500.42 MB - Synapse Storage) [md5](#)


Synapse ID: syn2246875


Conditions for use: None ([change](#))

DOI: ([create DOI](#))

Annotations ([show](#))

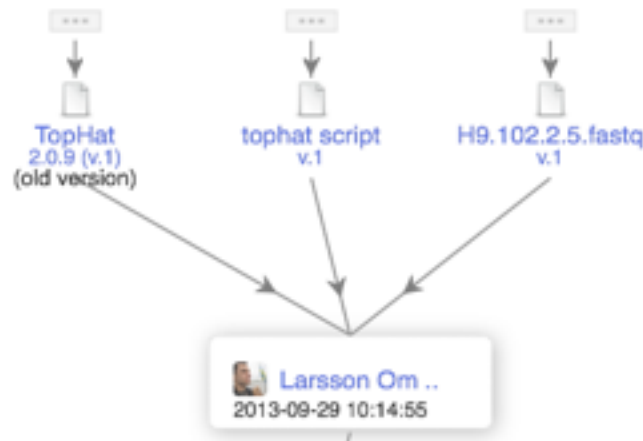
File History ([show](#))

 [Share](#)

 [Tools](#) ▾

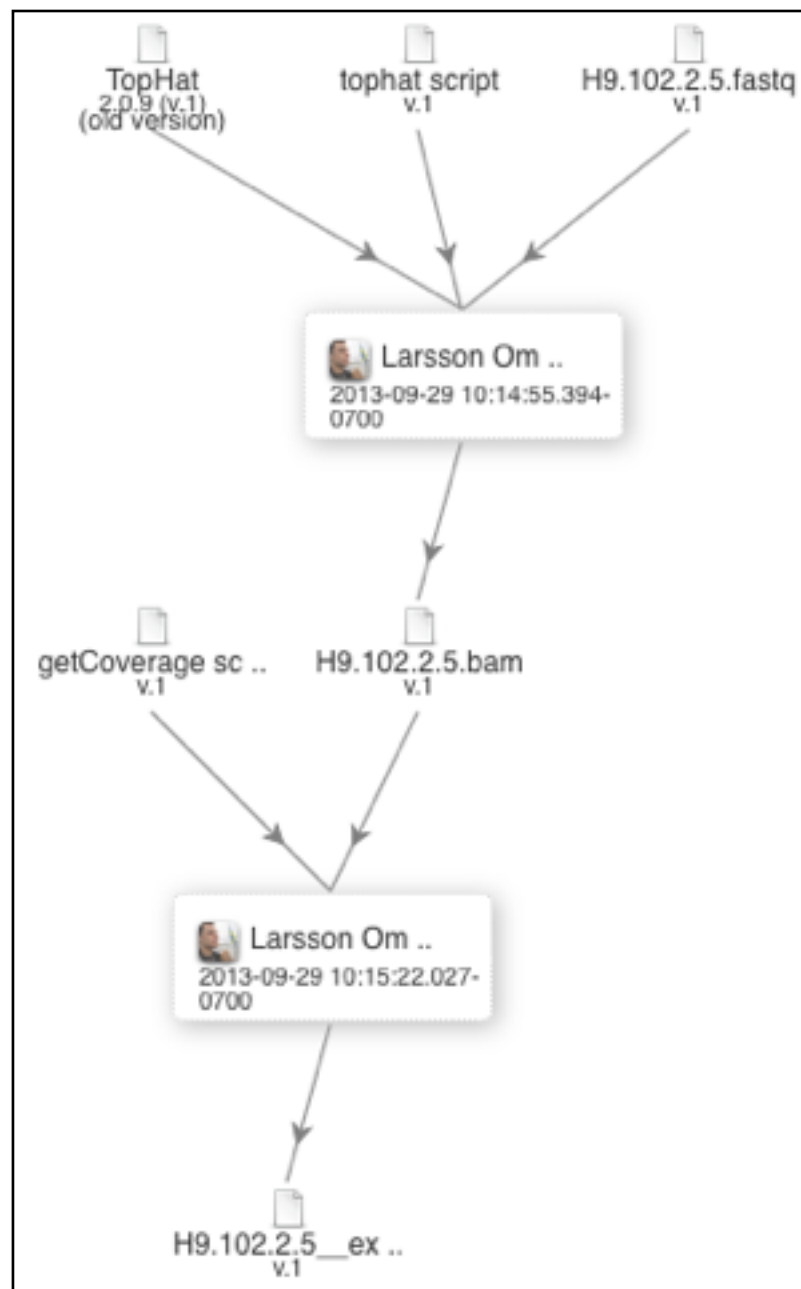
Preview

Provenance

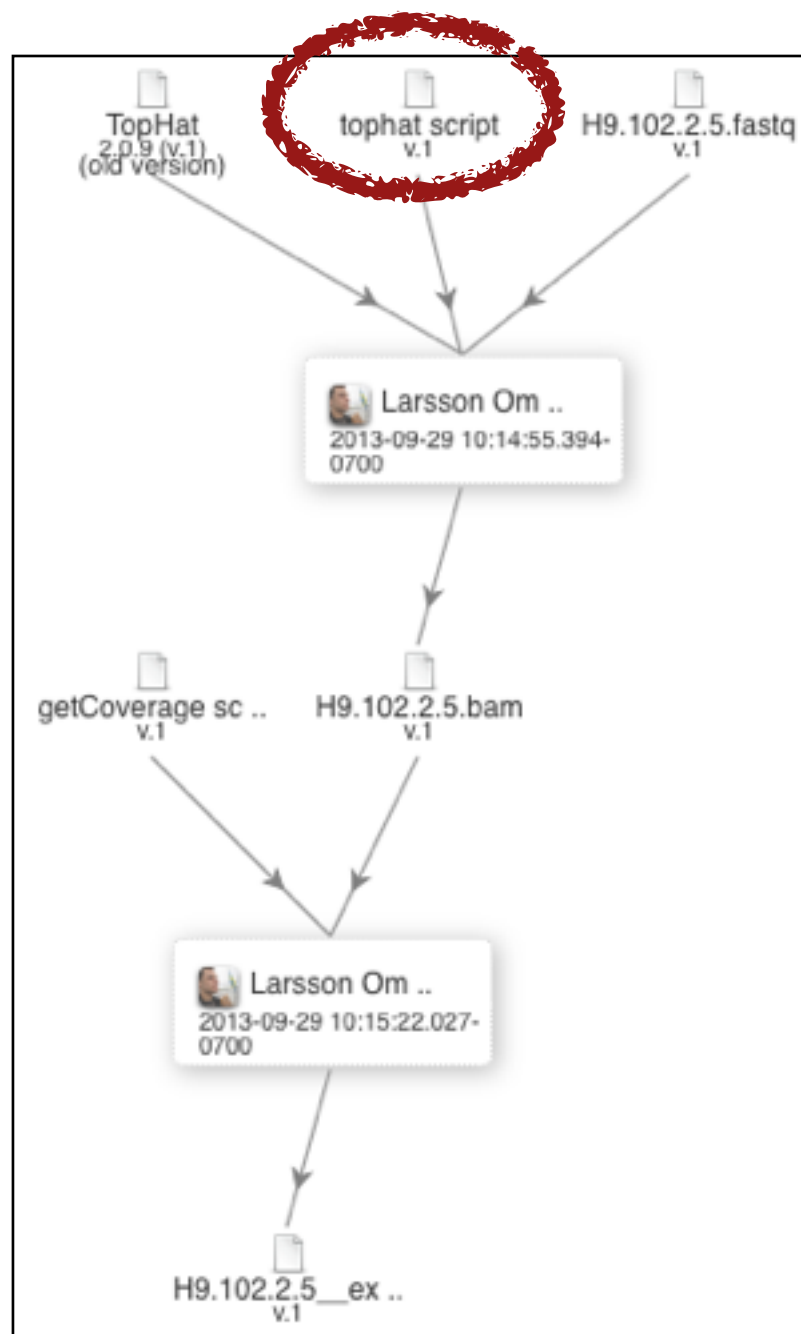


```
graph TD; A[TopHat 2.0.9 (v.1) (old version)] --> D[Larsson Omberg 2013-09-29 10:14:55]; B[tophat script v.1] --> D; C[H9.102.2.5.fastq v.1] --> D;
```

Sequencing Pipelines developed at Cincinnati Children's Hospital



All Code used to generate data downloadable



tophat script

File: run_samp.sh (496 bytes - Synapse Storage) *md5*

Synapse ID: syn2246674

Conditions for use: None ([change](#)) [report issue](#)

DOI: ([create DOI](#))

Annotations ([show](#))

File History ([show](#))

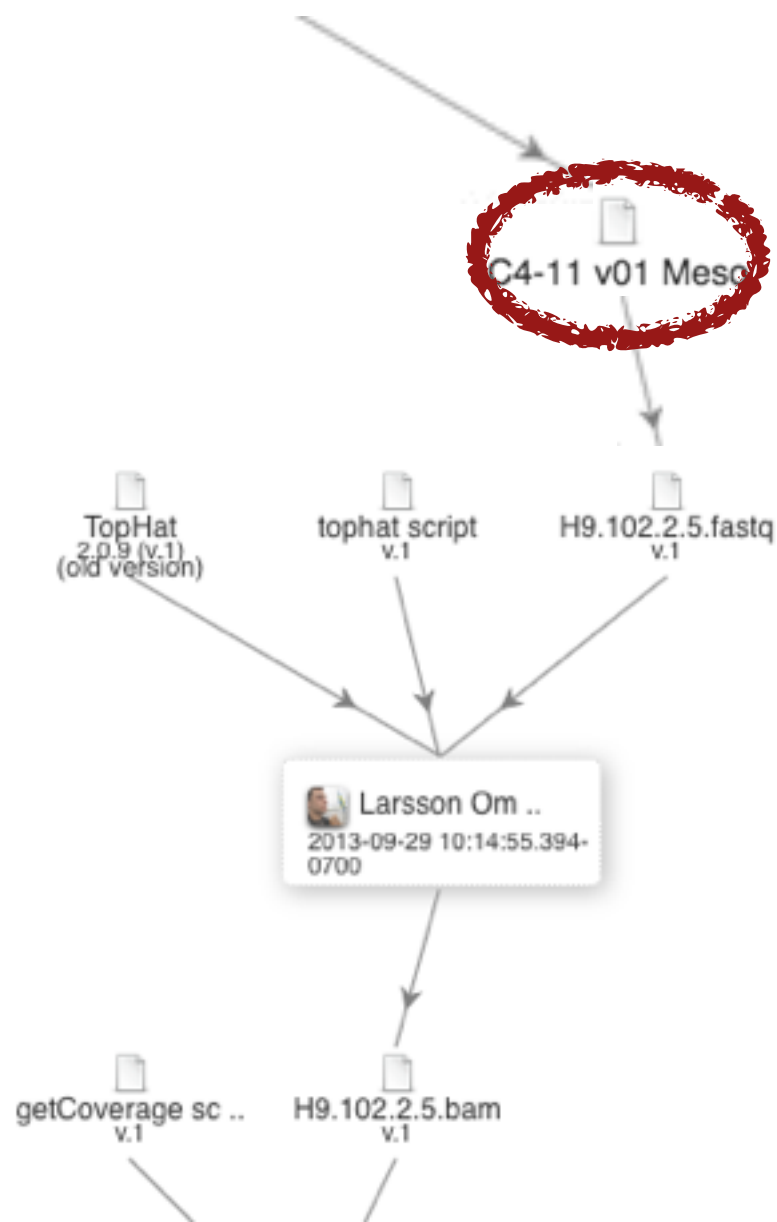
Preview

```
#BSUB -q nextgen

cd $DIR
module load tophat/2.0.9
tophat -o $SAMPLE -p 8 -G /data/illumina_data1/Genomes/GRCh37/annot/GRCh37_ucsc.gtf /data/illumina_data1/Genomes/GRCh37/ref/GRCh37 $FASTQ
mv $SAMPLE/accepted_hits.bam ../bam2/$SAMPLE.bam
cd ../bam2
samtools index $SAMPLE.bam
EOF
```

Experimental Protocols Linked to Datasets

Sample



C4-11_v01 Mesoderm Differentiation

File: C4-11_v01 Mesoderm Differentiation Protocol.pdf (29.763 KB - Synapse Storage) *md5*

Synapse ID: syn2512371


Conditions for use: None ([change](#)) [report issue](#)

DOI: ([create DOI](#))

Annotations ([show](#))

File History ([show](#))

Page 1 of 4

 **Cincinnati Cell Characterization Core Standard Protocol**

TITLE: Mesoderm Differentiation Protocol

PROTOCOL #: C4-11_v01

APPROVAL: _____ DATE: _____
Lab Director

This protocol was adapted from: Zhang, Jianhua, et al. "Extracellular Matrix Promotes Highly Efficient Cardiac Differentiation of Human Pluripotent Stem Cells: The Matrix Sandwich Method." *Circulation Research* (2012).

1. Media and Reagents

- 1.1. mTeSR1 (Stem Cell Technologies Cat# 05873)
- 1.2. RPMI 1640 (Invitrogen, 11875-119)
- 1.3. DMEMF-12 (Invitrogen, Cat# 11330-032)
- 1.4. Versene (Life Technologies, Cat# 15040-066)
- 1.5. bFGF 1µg/ml (Invitrogen Cat# P800024)
- 1.6. Activin A 100ng/µl (PeproTech Cat# AF-120-14E)
- 1.7. BMP-4 50µg/ml (PeproTech, Cat# AF-120-CSET)
- 1.8. B27 supplement minus insulin, 50x Stock (Life Technologies, Cat# 0050129SA)
- 1.9. Matrigel (BD, Cat# 354277)
- 1.10. ROCK Inhibitor, reconstituted to 1mM stock (Millipore, Cat# SCM073)
- 1.11. Triazol Reagent (Ambion, Cat # AM9718)
- 1.12. DPBS (Corning, Cat# 21-031-CV)
- 1.13. Brachyury - APC (R&D, Cat#DC0851A)
- 1.14. Oct 3/4 - PE (BD, Cat# 560186)
- 1.15. IgG1K Isotype Control - PE (BD, Cat# 559320)
- 1.16. Mouse IgG2B Isotype Control -APC (R&D, Cat# IC0041A)
- 1.17. Accutase (Innovative Cell Technologies, Cat# AT-104)
- 1.18. Fia/Perno Kit (BD 554772)
- 1.19. FACs Tubes (BD Falcon, Cat# 352054)
- 1.20. Staining buffer (2% FBS in DPBS)
- 1.21. Blocking Buffer (2% HSA, 1%TVIG in DPBS)
- 1.22. IVIG 10% (Baxter)
- 1.23. HSA 25% (Baxter)

2. Equipment and Materials Required

- 2.1. Incubator at 37°C, 5% CO₂
- 2.2. Biological Safety Cabinet
- 2.3. Centrifuge
- 2.4. Sterile glass serological pipets
- 2.5. 6-Well tissue plates
- 2.6. Pipet aid

Meta Data about samples defined by ontologies stored in query-able data structures

Progenitor Cell Biology Consortium (PCBC)

Wiki Files Tables

Tables Clinical Meta data

Clinical Meta data ☆

Synapse ID: syn2470916
DOI: (create DOI)
Annotations (show)

Table Schema

SELECT * FROM syn2470916

Edit Rows Download

order PCBC Cell Line Name Host species C4 Cell Line ID Profiled Originating Lab ID Public Data? Cell Type Cell Line Type Cell Type of Origin Cell Line of Origin

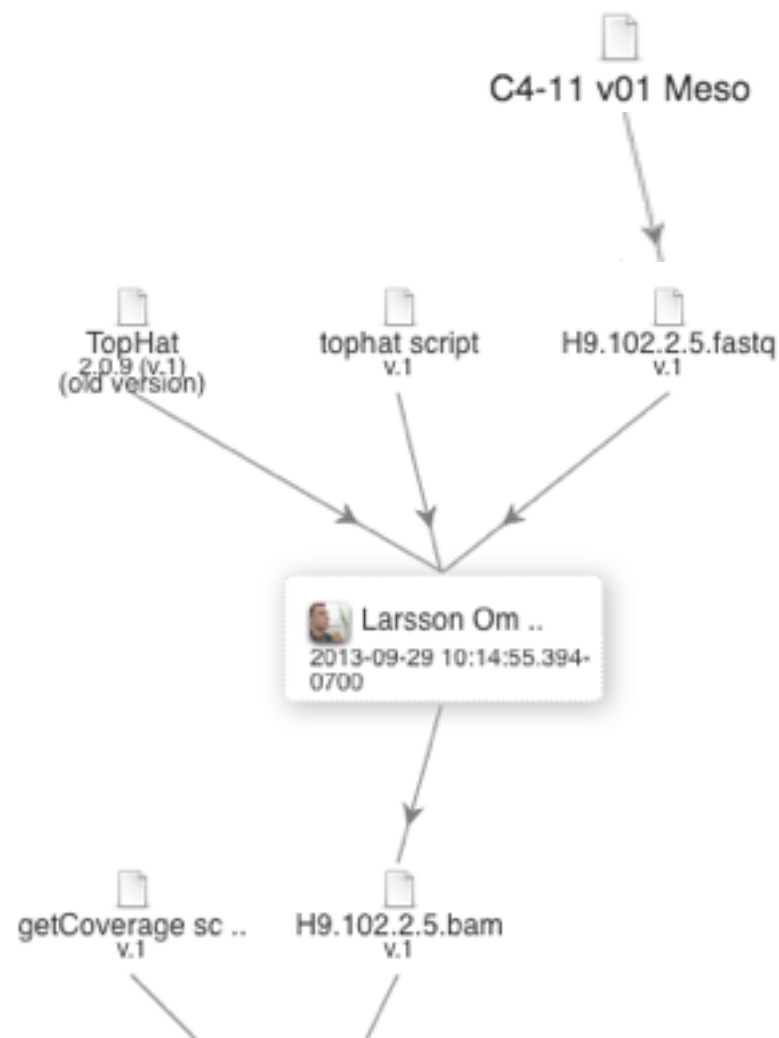
1.0	NaN																	
2.0	NaN																	
19.0	NaN																	
3.0	PCBC01ha20																	
4.0	PCBC01ha20																	
5.0	PCBC01ha20																	
6.0	PCBC01ha2011070104	human	SC11-005	NaN	CHOP_WT2.1	yes	PSC	IPSC	fibroblast	NaN	skin	lentivirus	OSKM	Cre-excised	NaN	NaN	childhood	NaN
7.0	PCBC01ha2011070105	human	SC11-006	NaN	CHOP_WT2.2	yes	PSC	IPSC	fibroblast	NaN	skin	lentivirus	OSKM	Cre-excised	NaN	NaN	childhood	NaN

Donor Life Stage Race

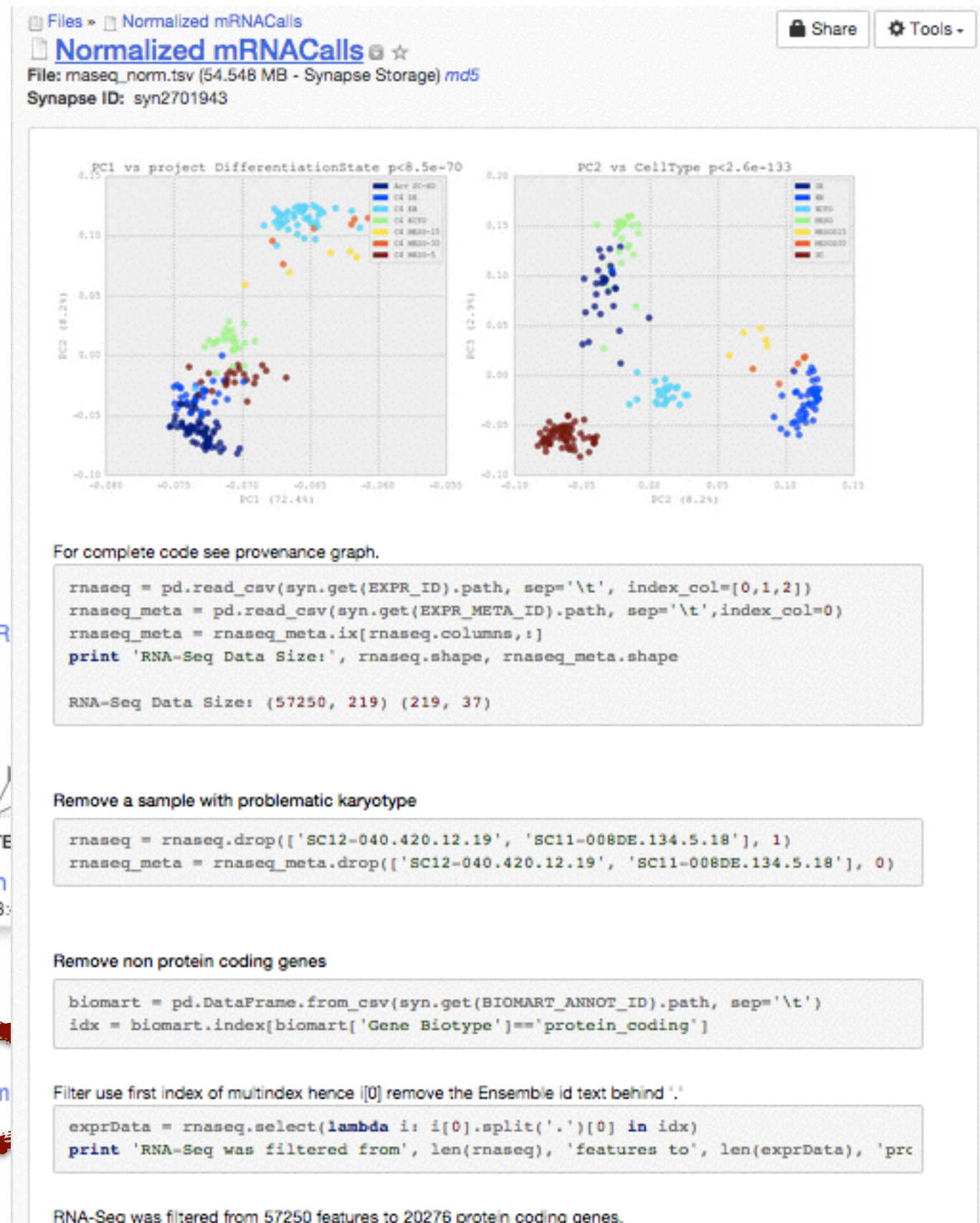
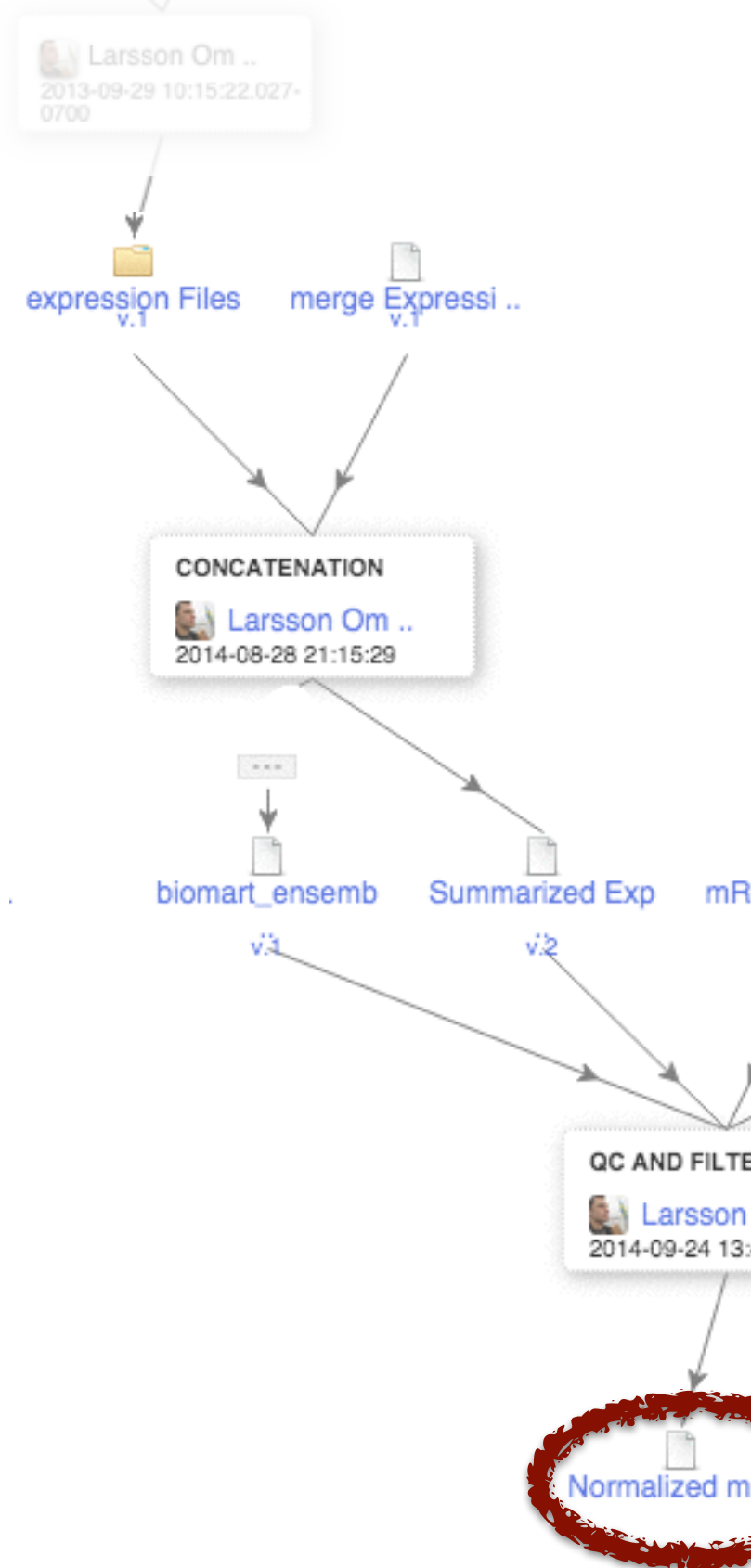
embryo	NaN
NaN	NaN
adult	NaN
childhood	white
childhood	white
childhood	white

Save Cancel

Lets return to the sequence data...



Lets return to the sequencing data...and go beyond



Synapse

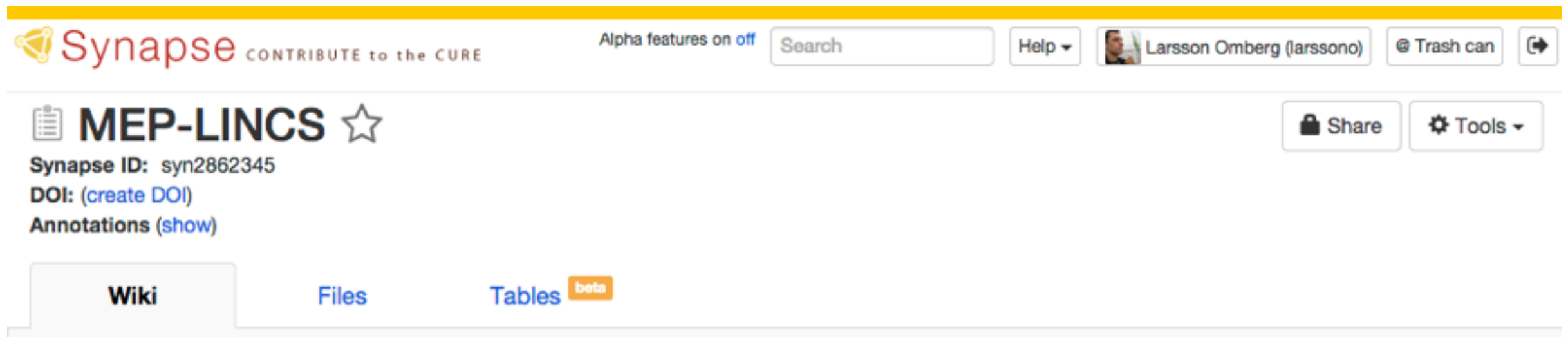
enabling large-scale collaborative science

Notes about security and Access Restrictions

- Access Restrictions
- Governance
- Data can be stored externally accessible by URL/
sftp/S3 etc.

Synapse

enabling large-scale collaborative science



Existing Resources

- Protocols
- Pre-existing data
- Preliminary Analysis
- Exploratory Analysis tools

Synapse

enabling large-scale collaborative science

Synapse Help:

General: <https://www.synapse.org/#!Help:GettingStarted>

R: <https://www.synapse.org/#!Help:RClient>

Python: <https://www.synapse.org/#!Help:PythonClient>
<http://python-docs.synapse.org/>

Command line: `synapse -h`

Synapse Vignettes:

<https://www.synapse.org/#!Synapse:syn2472293>

<https://github.com/Sage-Bionetworks/synapseTutorials>